BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT
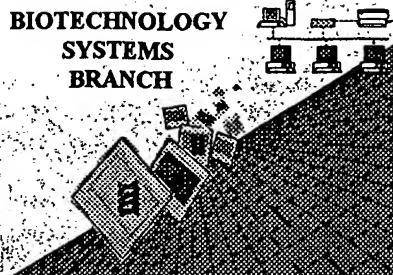
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___10/003,674___

Source: ___OIPE___

Date Processed by STIC: ___12/14/01___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
 PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
 PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
       http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by the treatment given to all mail coming via the Brentwood Mail Facility.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
    1911 South Clark Street, Crystal Mall One, Sequence Information, Arlington, VA 22202
              Or
    U.S. Patent and Trademark Office, 2011 South Clark Place, Customer Window, Box Sequence, Crystal Plaza Two,
    Lobby, Room 1B03, Arlington, Virginia 22202
4. Federal Express Delivery, 2011 South Clark Street, Crystal Plaza 2, Room 1B03-Mailroom, Box Sequence,
    Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 10\003,674

1 _____ Wrapped Nucleics
   Wrapped Aminos
   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length
   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino Numbering
   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII
   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length
   Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0 "bug"
   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences (OLD RULES)
   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   This sequence is intentionally skipped

   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences (NEW RULES)
   Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
   <210> sequence id number
   <400> sequence id number
   000

9 _____ Use of n's or Xaa's (NEW RULES)
   Use of n's and/or Xaa's have been detected in the Sequence Listing.
   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213> Response
   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220>
   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
   (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0 "bug"
   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING   DATE: 12/14/2001
PATENT APPLICATION: US/10/003,674 TIME: 11:10:29

Input Set : **A:\Es.txt**
Output Set: **N:\CRF3\12142001\I003674.raw**

Does Not Comply
Corrected Diskette Needed

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

```
       4 <110> APPLICANT: Wolfe, M. Michael
       5         Tseng, Chi-Chuan
       6         Neville, Linda
       8 <120> TITLE OF INVENTION: Specific Antagonists for
       9         Glucose-Dependent Insulinotropic Polypeptide (GIP)
      12 <130> FILE REFERENCE: 50128/002002
C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/003,674
C--> 15 <141> CURRENT FILING DATE: 2001-10-23
      17 <150> PRIOR APPLICATION NUMBER: 60/032,329
      18 <151> PRIOR FILING DATE: 1996-12-03
      20 <160> NUMBER OF SEQ ID NOS: 14
      22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
```

-Misaligned amino numbering
throughout — see error
Summary sheet #3.

ERRORED SEQUENCES

```
      24 <210> SEQ ID NO: 1
      25 <211> LENGTH: 30
      26 <212> TYPE: PRT
      27 <213> ORGANISM: Homo sapiens
      29 <400> SEQUENCE: 1
      30 Tyr Ala Glu Gly Thr Phe Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys 1
E--> 31 5                     10                   15      Ile His Gln Gln Asp Phe Val Asn
E--> 32 Trp Leu Leu Ala Gln Lys           20              25                  30
      34 <210> SEQ ID NO: 2
      35 <211> LENGTH: 24
      36 <212> TYPE: PRT
      37 <213> ORGANISM: Homo sapiens
      39 <400> SEQUENCE: 2
      40 Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys Ile His Gln Gln Asp Phe 1
E--> 41 5                     10              15      Val Asn Trp Leu Leu Ala Gln Lys
E--> 42 20
      44 <210> SEQ ID NO: 3
      45 <211> LENGTH: 15
      46 <212> TYPE: PRT
      47 <213> ORGANISM: Homo sapiens
      49 <400> SEQUENCE: 3
      50 Lys Ile His Gln Gln Asp Phe Val Asn Trp Leu Leu Ala Gln Lys 1               5
E--> 51 10                    15
      53 <210> SEQ ID NO: 4
      54 <211> LENGTH: 9
      55 <212> TYPE: PRT
      56 <213> ORGANISM: Homo sapiens or Rattus norvegicus
      58 <400> SEQUENCE: 4
E--> 59 Ile Ser Asp Tyr Ser Ile Ala Met Asp 1               5
      61 <210> SEQ ID NO: 5
      62 <211> LENGTH: 21
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RAW SEQUENCE LISTING   DATE: 12/14/2001
PATENT APPLICATION: US/10/003,674   TIME: 11:10:29

Input Set : **A:\Es.txt**
Output Set: **N:\CRF3\12142001\I003674.raw**

```
   63 <212> TYPE: PRT
   64 <213> ORGANISM: Homo sapiens
   66 <400> SEQUENCE: 5
   67 Tyr Ser Ile Ala Met Asp Lys Ile His Gln Gln Asp Phe Val Asn Trp 1
E--> 68 5                10              15      Leu Leu Ala Gln Lys              20
   70 <210> SEQ ID NO: 6
   71 <211> LENGTH: 3
   72 <212> TYPE: PRT
   73 <213> ORGANISM: Homo sapiens or Rattus norvegicus
   75 <400> SEQUENCE: 6
E--> 76 Ile Ser Asp 1
   78 <210> SEQ ID NO: 7
   79 <211> LENGTH: 30
   80 <212> TYPE: PRT
   81 <213> ORGANISM: Rattus norvegicus
   83 <400> SEQUENCE: 7
   84 Tyr Ala Glu Gly Thr Phe Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys 1
E--> 85 5                10              15      Ile Arg Gln Gln Asp Phe Val Asn
E--> 86 Trp Leu Leu Ala Gln Lys              20                  25              30
   88 <210> SEQ ID NO: 8
   89 <211> LENGTH: 24
   90 <212> TYPE: PRT
   91 <213> ORGANISM: Rattus norvegicus
   93 <400> SEQUENCE: 8
   94 Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys Ile Arg Gln Gln Asp Phe 1
E--> 95 5                10              15      Val Asn Trp Leu Leu Ala Gln Lys
E--> 96 20
   98 <210> SEQ ID NO: 9
   99 <211> LENGTH: 15
  100 <212> TYPE: PRT
  101 <213> ORGANISM: Rattus norvegicus
  103 <400> SEQUENCE: 9
  104 Lys Ile Arg Gln Gln Asp Phe Val Asn Trp Leu Leu Ala Gln Lys 1                    5
E--> 105 10              15
  107 <210> SEQ ID NO: 10
  108 <211> LENGTH: 21
  109 <212> TYPE: PRT
  110 <213> ORGANISM: Rattus norvegicus
  112 <400> SEQUENCE: 10
  113 Tyr Ser Ile Ala Met Asp Lys Ile Arg Gln Gln Asp Phe Val Asn Trp 1
E--> 114 5                10              15      Leu Leu Ala Gln Lys              20
  116 <210> SEQ ID NO: 11
  117 <211> LENGTH: 42
  118 <212> TYPE: PRT
  119 <213> ORGANISM: Homo sapiens
  121 <400> SEQUENCE: 11
  122 Tyr Ala Glu Gly Thr Phe Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys 1
E--> 123 5                10              15      Ile His Gln Gln Asp Phe Val Asn
  124 Trp Leu Leu Ala Gln Lys Gly Lys              20              25
```

```
                    RAW SEQUENCE LISTING              DATE: 12/14/2001
                    PATENT APPLICATION:   US/10/003,674   TIME: 11:10:29

                    Input Set : A:\Es.txt
                    Output Set: N:\CRF3\12142001\I003674.raw

E--> 125 30         Lys Asn Asp Trp Lys His Asn Ile Thr Gln      35                    40
     127 <210> SEQ ID NO: 12
     128 <211> LENGTH: 42
     129 <212> TYPE: PRT
     130 <213> ORGANISM: Rattus norvegicus
     132 <400> SEQUENCE: 12
     133 Tyr Ala Glu Gly Thr Phe Ile Ser Asp Tyr Ser Ile Ala Met Asp Lys 1
E--> 134 5                   10                  15      Ile Arg Gln Gln Asp Phe Val Asn
     135 Trp Leu Leu Ala Gln Lys Gly Lys         20                  25
E--> 136 30         Lys Asn Asp Trp Lys His Asn Ile Thr Gln      35                    40
     138 <210> SEQ ID NO: 13
     139 <211> LENGTH: 10
     140 <212> TYPE: PRT
     141 <213> ORGANISM: Homo sapiens or Rattus norvegicus
     143 <400> SEQUENCE: 13
E--> 144 Asp Phe Val Asn Trp Leu Leu Ala Gln Lys 1                5                    10
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/003,674

DATE: 12/14/2001
TIME: 11:10:30

Input Set : **A:\Es.txt**
Output Set: **N:\CRF3\12142001\I003674.raw**

```
L:14  M:270 C: Current Application Number differs, Replaced Current Application Number
L:15  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:31  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:32  M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:8 SEQ:1
L:41  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:42  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
L:42  M:252 E: No. of Seq. differs, <211>LENGTH:Input:24 Found:8 SEQ:2
L:51  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:51  M:252 E: No. of Seq. differs, <211>LENGTH:Input:15 Found:0 SEQ:3
L:59  M:252 E: No. of Seq. differs, <211>LENGTH:Input:9 Found:0 SEQ:4
L:68  M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:0 SEQ:5
L:76  M:252 E: No. of Seq. differs, <211>LENGTH:Input:3 Found:0 SEQ:6
L:85  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:86  M:252 E: No. of Seq. differs, <211>LENGTH:Input:30 Found:8 SEQ:7
L:95  M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:96  M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:96  M:252 E: No. of Seq. differs, <211>LENGTH:Input:24 Found:8 SEQ:8
L:105 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:105 M:252 E: No. of Seq. differs, <211>LENGTH:Input:15 Found:0 SEQ:9
L:114 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:0 SEQ:10
L:123 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:125 M:252 E: No. of Seq. differs, <211>LENGTH:Input:42 Found:8 SEQ:11
L:134 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:136 M:252 E: No. of Seq. differs, <211>LENGTH:Input:42 Found:8 SEQ:12
L:144 M:252 E: No. of Seq. differs, <211>LENGTH:Input:10 Found:0 SEQ:13
```